

QY 1138 TGGCGCAAGGAGACGAAGACTGAAACAATCGACCGAGGTACAGTGGAGGAGTATC 1197
Db 205 ACTCGCAGAGCTTACCAACTCTGCAGAACGCCGACATATTCCCTGCTGAGGAAATGTT 264
QY 1198 AGATTCTTGAGATGATGATGCTCGGGAAAGGAGTATCCCTGATATGAACTTAPGC 1257
Db 265 ACGCTTTCAGACTGAGATGAGTCTGAGCTGAGGATCTCTGACTTCACITGCA 324
QY 1258 CAGTGGGTACTGGAGGAGCTGGAGCATCTTCAGAGAAGTGTCACTG 1308
Db 325 CAACTGGATCTTGAGAGATGCTTCAACCTGACACTCTACAA 384
QY 1347 GTGGAATGTAAGGACTACAGACUTTGAGTGAATCATGGGGTTGGCTCTG 1406
Db 445 GTAGAGCTTACCAAGGTATGACCTCTGATAGTTGAGGATTGGATGCTTG 504
QY 1407 AGGTCCTAGGATGAGACAGGGTACAGATTAGATCAAGAATGGAAAGACTTT 1466
Db 505 CATTGTTGTTGTTGAGGATGCTGATCTACAGTACAGT 564
QY 1467 GTTTCCCTAGTGAAGGGACCAACCCCGTTACAGGAGCTTAAAGGTT 1526
Db 565 GATTTCCTAGGAGGATGCTGATCTACAGTACAGT 624
QY 1527 TGGCTACTATGGACAATCTACCCATACTGAGGCTGCGGTTGGACCAACT 1586
Db 625 TGGATCACCATGGCACTCTTACCTGTGATGCTTCAGTCAGAGCATGATA 684
QY 1587 CGGAGTCTGAGTCTGCTACTTCAAGGCTGGTCAAGTTTATCCAGGG 1646
Db 685 CGCAGCCTGTCATCGTACAGGTTCTCCAGGTRTGACCAAGTACTCTCCAGG 744
QY 1647 TCTACAGGCACTGTCACTAATCTGTGATGAGATGATGTCGATGGCCCTAAGGA 1706
Db 745 ATTACAGGGATGTCACTAATCTGTGATGAGATGATGTCGATGGCCCTAAGGA 804
QY 1707 CTCCGCTTAAAGAAAGATGTCCTGAGGAGATCTAACCTCCACCGATA 1766
Db 805 CTCCGCCAACATAAAATGGCTGTCCTCAGGGTAAAGTCAATGACACCTCTCT 864
QY 1767 ATGCCCTGTGATGATGCACTCTGTGGTACATGAACTGGGGCTGACAAGGCAAGAG 1826
Db 865 ATACTCTCTGATCTGCTGATGAGTCAAAACCTGGGTCACAATACCGAAG 924
QY 1827 AAGGTAGAGGAGGCAATGCTGGGGGGTGTGAGCCATTCTGAAGTTGAGA 1886
Db 925 AGACGACGAGGGCTCTGTGATAGGGCTGGTGTGAGTCAAAACCTGGGTCACAATACCGAAG 984
QY 1887 GTCCGCTCAAGAAAGTAGGGTACGGGAGATGATGGATGATCACTGCGCA 1946
Db 985 GTCCTCACTCAATCTGACTCGACCAAGCACTGGATATGACACTACAC 1044
QY 1947 TGTGAGTCTGAGTTGACATGGTGGCCACTTCACTGACATGGATATGAGCACT 2006
Db 1045 TGCCTAATCTGAGTTGACATGGTGGCCACTTCACTGACATGGATATGAGCACT 1104
QY 2007 TGTGAGTCTGAGTTGACATGGTGGCCACTTCACTGACATGGATATGAGCACT 2066
Db 1105 AGACGAGGAGCTACATCCCTCTCCCTGAGGTCACAGGATATCGAGGA 1164
QY 2067 AGAACATGACTCAAGCTGGCTGAAAGTCTTATTGAGGAGCTGGCAACT 2126
Db 1165 GATAACATGATTTAGGCTCTGAGTGGACGCTCCTACATGAGACGCTCACCATA 1224
QY 2127 GAGGAGTAGTACACCGAGGAGCTAACATAGAGATGATGAGACATGATA 2186
Db 1225 GATGAGGAGCAGCTCTTGAGAGCT-----GTTGAGTGGATGAGAT 1275

RESULT 3
US-10-088-384a-27.rn1
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHIEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 34472/114 IMPU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: pTZ9gt-F18
 US-08-232-463-14

Query Match 2.9%; Score 90; DB 1; Length 7218;
 Best Local Similarity 4.5%; Pred. No. 1, 4e-15;
 Matches 18; Conservative 18; Mismatches 133; Indels 0; Gaps 0;
 Qy 50 AGCCGCCATGCTTCCCTACAACCTCACTCGAACCGCCGCTCTCACTACT 109
 Db 1053 AGGAGCTGGATYY 1112

Qy 110 CGGCTTCATCCTCTCATGCCTTCCTACAACCTCACTCGAACCTCGATATCACTCGAGC 169
 Db 1113 YYY 1172

Qy 170 TCGGCCCTCACCCCTCTCCATCGTACACGCCGCTCTCTCTCCAAAGAACAC 229
 Db 1173 YYY 1232

Qy 230 TCGAGCTCTGATTCACTCACTCGACCTCTGACCTCTACCAAGCGGGCTCACACTCTAGC 289
 Db 1233 YYY 1292

Qy 290 TCTTAACCCTGACCACTTCACCTCAACCAATCAATGTTTCTCCATTAAG 349
 Db 1293 YYY 1352

Qy 350 CTTGACATACTGAGCGCTGAGACACTATCACCTTCAGCTCTGATCTCATCGT 409
 Db 1353 YYY 1412

Qy 410 CCAACACGGTGCTTCATCCCCAGAAGCTGTCACTCCT 453
 Db 1413 YYY 1456

RESULT 4
 US 09-072-596-323
 Sequence 323 Application US/09072596
 ; Patent No. 6458366
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Steiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Meto, Antonia
 APPLICANT: Houghton, Raymond
 APPLICANT: Verdick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Ledes, Michael J.
 APPLICANT: Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESSE: SEED and BARRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 COMPUTER TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Makri, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 323:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1166 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 US-09-072-596-323

Query Match 2.0%; Score 63.8; DB 3; Length 1166;
 Best Local Similarity 26.7%; Pred. No. 3.2e-08;
 Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;
 Qy 2 TCATATTCGACCTCTCTCTCTCTCATCAAAGACACACAGCCGCGATCG 61
 Db 373 KSAAMTSKMGNGTSTYCTWYCNNGASATMYNCNCSCCGGWAKSWSWYCCCHGTC 432
 Qy 62 CTTCCTCTCAACCTCTACTCGACCCGCGCTCTACTACTCGCTCATCGC 121
 Db 433 TYCCMOWCSSGGYCYCTCANNCCACCGTGNYTYCCCTCCKMKTCTCAYTCMTCGGTWCC 492

Qy 122 TCTCATGCCATCTCTCACTACACTCGACCTCGGGATAPTCACTCGAGCTGCCGCTTC 181
 Db 493 INTMMNNCCSNCRYCTCAMCNCTSKGKACCNATWYCNCSCAKNM 552

Qy 182 ACCGCTCTCATCTCACCCGCTCTCCCTCTCCAGAAACACTCGAGCTCTCCA 241
 Db 553 TCCCTONCCYTNNNCAMCMCSCTCTMCMACTCKCCGGYCKNCMTCCTCKCC 612

Qy 242 TTCACTACTGACCTTACCCAGGCGGCTCACCACTCTAGCTTAACCACTC 301
 Db 613 NMAACKKTCYCWNCWYCWYCKCKCAGWYKAMCTCCWACTCTMNTTCCTCNCKCCM 672

Qy 302 GACCACCTCACCATCACCATCAATCTTCTCTCCATTAAGCTGACATCTC 361
 Db 673 KACKKNTCTCWCSCCCCCACAKAYMCYAWCMWTCCTCMCTKAGSCCCYCNYYCMM 732

Qy 362 GACCGCTGACACTTATCACCTTCAGCTCTCATCTCTCATGTTCAACACCGCT 421
 Db 733 CWCMTCWTWNKACNCTNTCTCTCTCTCTMMTMACKCWNNTNCCKSGACCYCTCAC 792

Qy 422 CTCTATCCCAACGAAAGCTGTGATCACCTCTACCATCACAGGACTGATCA 481
 Db 793 TRMKCCWMTCCTTMKCCYMWCTCCKMKXNCCTCCNCTMCCKYCTCTCNMRYCY 852

Qy 482 GCAACCAACTCGACCTCGCTCTGACCATGACTGATCTCTCTCACCA - 540
 Db 853 YYAKCAKCNMCTCCCAKMKACTRKTCCTCCCACOMKSACNCCKCCWCCCTCTCATCWC 912

Qy 541 TCTCTCATCTCCCTACTGACCCACCTGGGCTCTGGCTCCACATCCATTAAAG 600
 Db 913 TCTCWTYARCTKCTCWTWNKACNCTCTCTCTMMTMACKCWNNTNCCKSGACCYCTCAC 972

Qy 601 CTCACTGATGTCAGAGAGAGAGTCAACCAACGCCAGTGAACCGCGTT 660
 Db 973 NYCTCWTWKGTYCKCCKCTMCKCNMCMRWTCTCCKKCCNCCKNCCKMCKMCT 1032

QY 661 CCCTCTACACATTCACACTCGACCACGGTGTACCCATCTCCACACCGCT 711
Db 1033 CTCCWMMTCCWCCATCTMMKSTCTCWCNCNTCCCTCNKCYNNTKCY 1083

RESULT 5
US-09-072-967-32B
; Sequence 32B, Application US/09072967
; Patent No. 6592877
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Nieto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121-411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4300
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 32B:
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-072-967-32B

Query Match 2.0%: Score 63.8; DB 4; Length 1166;
Best Local Similarity 26.7%; Pred. No. 3.2e-08;
Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;

QY 2 TCTATATTCGACCTCTTCTCATTTGCAATGAGACACAAAGGCCATCG 61
Db 373 KSAAMTSKMGGTSTYCTMNGGASTANTYAMCCCGGNAYCKSCWAKCCTCTCA 432
QY 62 CTTCTCCCTCACACTCTCACTGACCCGGCGCTCTCACTTACTCGCTTCATCG 121
Db 433 TCCCMCMGSGSGYCTCTCACACCTGTCAGCGCTGCTCCCTCTCCAGGGTWC 492
QY 122 TCTCATGCCATCTCACACTCTCACCTGACCTCGATCTGAGCTCGCGCTTC 181
Db 493 TTTMMNCCCSNCNYCTCAGTCATGCTGSKGCACCATMTCGSCAKMT 552
QY 182 ACGGCCTCTCATGTCAGCGCTGCTCCCTCTCCAGGAACACTCGAGCTCTCA 241
Db 553 TCCCTCTCTVTCNNCCAMCMCSCTCTMCMACTCKCCGGYCKCNOMYCCTCKKCA 612

QY 242 TTCACTCACTGACCTCTACCCAGCGACTCTACACTCTAACCTC 301
Db 613 NMAACCKTKYCWNCNMVCMTCCKCKGKAWYKOMTCMCTCWAETCTMNTTCCTCNKCCM 672

QY 302 GACCACCTCACATCACCACTCAAAATCGTTTCCTCCATAAGCTTGACATCTC 361
Db 673 KACKNNTCTCWSCCCCACAKAYWMTMTCMTCACSCCCYCNMCCM 732

QY 362 GACCGTGAACACTTATCACCTCAAGCTCCATCTCATGTTCCACACGGCTG 421
Db 793 TMMKCCMTCCTTCKMTCMKCNMTCMKNCCCTCMMTOMTCMTCXTCCTCNMHCY 852

QY 482 GCAACCAACTGACCTGCTCTCTGCTCCACTCATGTCACTCGATCTCTCACCA- 540
Db 853 YYAKCAKNMTCMCCANKMCAKTKTCCCACOKMSACNOKCCWCCCTCTATCWC 912

QY 541 TCTTCATCATCCTACTGACCAACGGTGTGCTGCTGCTGACCTGATGTTAAAG 600
Db 913 TCTCWCYATCTCKCTCKTCMTCMTCMTCMTCMTCMTCMTCMTCMTCMTCMTC 972

QY 601 CTCACTGATGTCAAAGAGAAGAGTGAAGCTCACCAACGGCTGACGGCTT 660
Db 973 NYCTCWCYACGTYCKCKCTCKMTCMTCMTCMTCMTCMTCMTCMTCMTCMTCMTC 1032

QY 661 CCCTCTACACATTCACACTCGACCACGGTGTACCCATCTCCACACCGCT 711
Db 1033 CTCCWMMTCCWCCATCTMMKSTCTCWCNCNTCCCTCNKCYNNTKCY 1083

RESULT 6
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHAFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLERPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; ZIP: 22313-0299
; COUNTRY: USA
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
ENZYME: 7210 KODAK BIOTECH

; ORGANISM: Human
US-09-949-016-16945

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ2GPT-F1s
US-08-232-463-14

	Query Match	Score	DB	Length
Qy	Best Local Similarity	47.7%	Pred. No.	7.1e-06
Db	Matches	240;	Conservative	Mismatches
89	CGCCGCCCTCTCACTTACTGCGCTCATGGCTCATGCCATCTCAACATACTCG	148		
25834	CCTCTTACTCACCCTCTACCCCTCTACCCCTCTACCCCTCTACCCCTCTACCC	28893		

US-08-658-136-2
RESULT: 8
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:

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(c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 22, 2005, 00:46:28 ; Search time 5565 Second(s)

(Without alignments)
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Title: US-10-088-384A-27

Perfect score: 3122

Sequence: 1 ttccatatttcgacccttcc.....atggagataggccttgtaaagca 3122

Scoring table: IDENTITY_NUC

Gapext 1.0

Searched: 7172129809 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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25: /cgns_6/prodata/2/pupnna/us10c_PUBCOMB.seq:*

26: /cgns_6/prodata/2/pupnna/us60c_PUBCOMB.seq:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-10-315-515-125

; Sequence 125, Application US/1031515

; Publication No. US20030166190A1

; GENERAL INFORMATION:

; APPLICANT: Wright, David A.

; APPLICANT: Voytas, Daniel F.

; TITLE OF INVENTION: NUCLEIC ACIDS RELATED TO PLANT

; TITLE OF INVENTION: RETROELEMENTS

; FILE REFERENCE: 08411-031001

; CURRENT APPLICATION NUMBER: US/10/315,515

; CURRENT FILING DATE: 2002-12-10

; PRIOR APPLICATION NUMBER: US 60/339,060

; NUMBER OF SEQ ID NOS: 168

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 125

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; US-10-315-515-125

Query Match

Best Local Similarity 69.2%; Pred. No. 3-5e-283;

Matches 1609; Conservative 0; Mismatches 610; Indels 105; Gaps 8;

Qy 847 ACTTAACTATTAAGCTTATCCTTGAGTTGGTCCTTGTAGTCATGACTAC

Db 8571 ACTTAACTATTAAGCTTATCCTTGAGTTGGTCCTTGTAGTCATGACTAC

Sequence 123, App

Sequence 124, App

Sequence 125, App

Sequence 126, App

Sequence 127, App

Sequence 128, App

Sequence 129, App

Sequence 130, App

Sequence 131, App

Sequence 132, App

Sequence 133, App

Sequence 134, App

Sequence 135, App

Sequence 136, App

Sequence 137, App

Sequence 138, App

Sequence 139, App

Sequence 140, App

Sequence 141, App

Sequence 142, App

Sequence 143, App

Sequence 144, App

Sequence 145, App

Sequence 146, App

Sequence 147, App

Sequence 148, App

Sequence 149, App

Sequence 150, App

Sequence 151, App

Sequence 152, App

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Sequence 154, App

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Sequence 156, App

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Sequence 172, App

Sequence 173, App

Sequence 174, App

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Sequence 176, App

Sequence 177, App

Sequence 178, App

Sequence 179, App

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Sequence 181, App

Sequence 182, App

Sequence 183, App

Sequence 184, App

Sequence 185, App

Sequence 186, App

Sequence 187, App

Sequence 188, App

Sequence 189, App

Sequence 190, App

Sequence 191, App

Sequence 24, Appl

Qy 1874 GAAAGTTGGAGTCGGCTCAGGAGTAGGGTACCGAGAATGATGGACTTGA 1933
Db 9725 GATAGCTTGCTGAGTCGCACTCATTCCTGCTGAGCTCGAGCGAGAATGATGA 9784
Qy 1934 TAATCTGGCCGAGTGTAGTTCTGAGTTACATGGTTCAGCCTCCACCGCTACAG 1993
Db 9785 GCACCTAGTCACTGGGATTCGGATTCGGATTCTGGAGTTCTAGTGCACATTAGTCG 9844
Qy 1994 GTTCGACCATCATGATTAATGCAACATCTTTCCTGATTAGCTACTAG 2053
Db 9845 GTTGAGCACTCACAGACAGAGGAGCTAACATCCCTCTCTAGCATGAGTCACAG 9904
Qy 2054 GATTCTGGAGGCCAGGACATGACTCAAGCCTGGCTTGGAGCTTATGAGATGCC 2113
Db 9905 GATAATAGAGSAGAGATACATGATTTAGCTGAGATTCAGCCTAGGAGTCACAG 9964
Qy 2114 CAGTCGCCAACATGAGGAGATAGTACACCCAGAGGCTACATAGAGAAGTGTGATGA 2173
Db 9965 CGCTCCGCCATATGAGGATGAGGATCATCTCTGAGACT-----GCCTGGATGG 10015
Qy 2174 GACATATGATATAGATGAGGGAGGTGAGACAGACATGATTCAGTGGACATAT 2233
Db 10016 GATGGATGAAATATAGGGCACTGAGTCAGTTCAGTGGACATAGCATGATCACITG 10075
Qy 2234 ACCTCCAGGGAGAACAGAGTTGAGGAGCTCACAGAACAGACAGCTGA 2293
Db 10076 ACCTCCAGGGAGAACAGAGCTGACTGAGCTCATTAATAATACAGTAATGCA 10135
Qy 2294 GAAGTGGTGAAGAACAGGATAAGTACTCCAAAGTGTCAAGGCTATCAAGTGTCT 2353
Db 10136 GAATGGTGTGAGAAGGAGAACAGCTGATGCCAATG-----TTTGAGCTCT 10186
Qy 2354 GAAGGAGAGATCAGCTGAGTGTCTCTTCAACTAACATTGCAATGACGCTCCCTCA 2413
Db 10187 GACAGATAAGCTGAGTGTCTCTCACCACCTGCTATTCCACAGTACAGCTCTAT 10246
Qy 2414 GAGACATCCCTGGAGGATATGACGC-----GCCGAGCTAGAGAGCAA 2461
Db 10247 GGAGATGCCATGAGTAATGACCTGGCACAGGGCTGAGCTAGGAGAG 10306
Qy 2462 GATTCTGCATTCCTCCCTGGAGAAGCATTCATCTGGAGCTGAGCTGTAATCTAGAGATAG 2521
Db 10307 AGTCCCACTATTCAGGCTTACATGAGCTGAGCTGAGCTGAGCTGAGCTGAG 10366
Qy 2522 GAGAACACATCACTGATAGCAGCAGGAGAACGAGCTTCAGCTGAGTGTGAGTT 2581
Db 10367 GAAGGCTACATCACTGATAGCAGC---AGATCAGCCCTCATTACTGGAGAGTC 10423
Qy 2582 ACCGGACCCGGCTGCTGGCCCATGAGAGAGCTGAGCTGAGCTGAGCCGCTG 2641
Db 10424 ACTCGACCGGGTACTGCGCCAGAGAGAGGTCAGTCTCGAGCTGAGCTG 10483
Qy 2642 TGGCCGCCACAGAGCTGATGAGATCGAGTACCCACAGTGTCTGAGCTGAGCATGG 2701
Db 10484 TGGCCGCCACAGAGCTGAGTGTCTGGAGTACCTGCTGGCTGAGCTGAG 10543
Qy 2702 CGGTGCGCTCTGGCTGGGCAATCACAGCAGGCTTACCTACACTGGTCT 2761
Db 10544 AGGTTCTCTATGGCCCTGGAGCAATCGACAGCAGGCTTACAGGAACTAGTC 10603
Qy 2762 ATTCGACTGAGSTAAGGCCCACTTCACTTACATATATATCATCTCTGATGTT 2821
Db 10604 CTTGCGACTGAGSTAAGGCCCACTTCACTTACATGTTCTGAGCTGAGCTT 10663
Qy 2822 CTT---TATTGTTCTGAGTGTGGATTCTGAGTACCTACCTGATGTTCTGAGCT 2878
Db 10664 TCTCATTTTCTGAGTGTGGATTCTGAGTGTGGATTCTGAGCTTCTGAGCT 10723
Qy 2879 CACAGTGGACTCTGTTGAGTGTGGGGAGGGCTCAGAA---GTTATGAGCTGTA 2936
Db 10724 CACAGTGGACTCTGTTGAGTGTGGGGAGGGCTCAGAGAGTGTGTGAGCTG 10783
Qy 2937 TATATTTTAACTCTGCTGATTCTCTANGGATAGAAAACCAAACAAATTAATT 2996
Db 10784 TATATTGTTGACTCTACATTCTCTAGGATAGAAAC-AAAATTCGAAATT 10842
Qy 2997 CAGAAATGATTTCAC---AAAAMAGAGTGTCTAGTGTGATCATTCATTAGTC 3053
Db 10843 CAGAAATGATTTCACAAAAAAAGAGTGTCTAGTGTGATCATTCACATTAGTC 10902
Qy 3054 AGTCTAGGTGTTCTTGTGATGATGATGGGATATGAGATAGGCC 3113
Db 10903 AGTCTAGGTGTTCTCTAGGATCTGATGATGGGATGAGATAGGCC 10962
Qy 3114 TTGTAAACA 3122
Db 10963 TTGTAAACA 10971

RESULT 4
US-10-315-515-121
; Sequence 121, Application US/10315515
; Publication No. US20030166190A1
; GENERAL INFORMATION:
; APPLICANT: Wright, David A.
; TITLE OR INVENTION: NUCLEIC ACIDS RELATED TO PLANT
; TITLE OF INVENTION: RETROELEMENTS
; FILE REFERENCE: 08411-031001
; CURRENT APPLICATION NUMBER: US/10/315,515
; CURRENT FILING DATE: 2002-12-10
; PRIORITY APPLICATION NUMBER: US 60/339,060
; PRIORITY FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO: 121
; LENGTH: 13894
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
DS-10-315-515-121

Query Match 32.9%; Score 1027.4; DB 16; Length 13894;
Best Local Similarity 68.6%; Pred. No. 1.2e-274;
Matches 1620; Conservative 0; Mismatches 626; Indels 117; Gaps 10;

Qy 820 TTAGATGTTGTTGGTTCTATTACTACATATTAAGTTRATCTTGAGTTCTG 879
Db 8630 TAATTGTTCTATGCTATCTCTGAGACTAACCTATGACATTGAGCTTGAGTCTA 8689
Qy 880 CTGTTTGTAGGTTCTATGAGTAACTACAGTGGAAATCTCTTGTGACCTGAT 939
Db 8690 AACCCCACAGGAAATCTGACATTAAGTGGCTCTCTGAGCTGACTAC 8749
Qy 940 AATGTCGATGAGCTAGTCCTGGTCCACTAGACCGGGAGGAGACATGTTAGG 999
Db 8810 AGTTTCG-----
Qy 8750 AACATGGATGAGACAGATCGCTCATCTCAAGGCCAGAGAGAACAGAA 8809
Db 1000 ACCTATGGATGAATTGAACTCTGCTGAGCTGAGCTGAGCTGAGCTGAG 1059
Qy 8834 GCGCAGAGAGAGGAGGATGAGAGAGGAGGAGGAGCTTATGAGGAGATCTGGAGAC 8893
Db 1120 GAGTATGAGCCAGAGCTGAGCTGAGGAGGAGGAGCTACTGAGCAATCTGAGCGGGTT 1179
Qy 8894 GAGTACATGCCATGAGACAGACTGCGAGAGCTACCAACATTCTGAGCCGACATATTG 8953
Db 1180 ACAGTGGAGGAGTACAGATCTTGTGAGTGTACTCTGGGAGCAGGATCCC 1239
Qy 8954 CCTGCTGAGGATATCTAGCTGGCTTCACTGAGTGTCTGAGCTGAGCTGAGCT 9013
Qy 1240 TCATATGAGACTTCTGAGCTGAGGAGCTGAGCTGAGCTGAGCTGAG 1299
Db 9014 TCTCGACCTACTGCGACACTCGGATCTGGAGATGTCAGCCACCTGACAAAGT 9073

Db 10589 TTCACTTCTTCCACTGAGGTAAGCGCCTCACTTCACCATGGATTACCGTCTGTGTGA 10648
 Qy 2816 TTGTTCTT--TATTGTTCAAGTGTGATGTTGCTCTGAGACTCTCTCCAAAGT 2872
 Db 10649 TTGTTCTCTCTTCTTGTCTGATGTTGCTGTGACTCTCTCCAAAGT 10708
 Qy 2873 TATTCAACAGCTGGACTGTGIGGATTAAGTTGGGGAGGCTCAGGA--GTATGTTG 2930
 Db 10709 TATTCAACAGCTGGACTGTGIGGATTAAGTTGGGGAGGCTCAGGAAGTGTG 10768
 Qy 2931 ATTGATAATATTTAAGTCGCATTCTAACGGATAGAAACCAAAA--- 2986
 Db 10769 ATTGTTATAATTTCAGTCGCATTCTAACGGATAGAAACCAAAA 10928
 Qy 2987 ---TAAATTGAGAAMATGATTCA---AAMAAAGAGTCTCTGTAGTGCA 3038
 Db 10829 ATTGTTGAAMATTCAAGAAMATGATTCTAACAAAAA--- 10888
 Qy 3039 TTACATTAGGATCAAGTCAGTCAAGTGTGCTATGGATAGGGAT 3098
 Db 10889 TCACATTAGGATCGAGTCAGITTCATTTGCAATGATGATAGGGAT 10948
 Qy 3099 ATGATGAGAGAAGCCGTGTAAGCA 3122
 Db 10949 ATGATGAGAGAAGCCGTGTAAGCA 10972

RESULT 6

US-10-315-515-124

; Sequence 124, Application US/10315515
 ; Publication No. US20030166190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wright, David A.
 ; APPLICANT: Voytas, Daniel F.
 ; TITLE OF INVENTION: NUCLEIC ACIDS RELATED TO PLANT
 ; TITLE OF INVENTION: RETROELEMENTS
 ; FILE REFERENCE: 08411-031001
 ; CURRENT APPLICATION NUMBER: US/10/315,515
 ; CURRENT FILING DATE: 2002-12-10
 ; PRIOR APPLICATION NUMBER: US 60/339, 060
 ; PRIOR FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 168
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 124
 ; LENGTH: 13320
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-315-515-124

Query Match 32.9%; Score 1025 6; DB 16; Length 13320;
 Best Local Similarity 68.9%; Pred. No. 3.7e-274;
 Matches 1620; Conservative 0; Mismatches 619; Indels 113; Gaps 11;

Qy 825 TTGTTCTTCTGTTCTATACATACATTTAACGTTCTTGAGTTGCTGTGTT 884
 Db 7962 TTGTTCTATCTATGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 8021
 Qy 885 TTAGGTTCTCATGTTAATCAGTGGAAATCTCTTGTGACCTGTATATGT 944
 Db 8022 CTACAGGAGATCTATGCAATTACAGTGGAGTCTCTGTTGATCTGACTACAT 8081
 Qy 945 GTATGAGCTAAGTCCTGTTCACTAGACCCAGTGAGGAAACATGTTTACAGCTA 1004
 Db 8082 CGATGAGACAGCTGTCATCTCAAGGCCAGAGGAACAGAGAATATGAAAGCTT 8141
 Qy 1005 TAGGATGAATTTGAACGCTTGCAGCTCGAGTAATCACAGAGAGCTGAACTCCTAG 1064
 Db 8142 CAG-----ANGAAAGCTGAGATGCCG 8165
 Qy 1065 AGGAAGAGGGCGATGTCGAGTAGATGATGATGATGAGGATATCAAACCTGATA 1124
 Db 8166 AGGAAGAGAGGAGGATGACAGAGAGGATGACGAGGAGATCTGGAGACGATA 8225

Qy 1125 TGACSCAGACTCATGCCAGAGGAGCAAGCTACTGACAATOCGAGGAGGTACGT 1184
 Db 8226 CATGCCATGACAGACTCGCAGAGCTTACACACTCTGACAAAGCCGAGATGCTTC 8285
 Qy 1185 GGAGGAGTATCGATCTGATTTGAGATGATGATGATGATGCTCGGGAGCAGAGTATCCTGTA 1244
 Db 8286 TGAGGATATGTTAGGCTTCAAGCTGATGATGATGATGATGCTCGAGAGTATCCTGTC 8345
 Qy 1245 TGAGACTTAGCCCAGTTGGGTACTGGAGGAGTGTGAGCATCTGTGAGAAGTGTCA 1304
 Db 8346 GACCTCACTGCACTACTGGATGTTGAGATGTTGAGCTGACCTGTTCAAGTTGCA 8405
 Qy 1305 TCTG-----ATAGGAGGAGACATCGAGTTCT 1333
 Db 8406 TCTGACACTCTGATGGCTATCGTAATGAGCTATGAGATGAGACATACATTCCT 8465
 Qy 1334 TTCCACATGCACTGGAAATGTTGAGCTACACAGGAGTGTGAGCTGATACATGG 1393
 Db 8466 CTCCACGCTGCAAGTAGAGCTTACACAGTGTGAGCTGAGCTGATACATGG 8525
 Qy 1394 GTTAGGCTCTTGAGCTCTAGTGATGAGACACGGGAGCAGATTGATCAGAATT 1453
 Db 8526 ATGGGATCTTGGATTTCTGTTGAGTGTGATGAGTATGATCATCACAGGAVT 8585
 Qy 1454 GAAAGACATGTTGTTCTAGGGAGGGACACCCAGGTTGACAGGAGA 1513
 Db 8586 GGAATGATTTGGCTCTAGGGAGGACTCTAACGAGGAGTCTAACGCAAGTA 8645
 Qy 1514 GCTTAAAGGATTGPGGGCTACTATGGAGAACTTACAGCTAACTGAGGTTCT 1573
 Db 8646 GTTGAAAGACTTGTGTTGATCACCATGTTGAGCTCTGAGCTCTGAGTCT 8705
 Qy 1574 GAGCACACAAATCCGGTCTGATGCTCTACTTCAAGGCTCTGGGTGCAATGTT 1633
 Db 8706 GAGCATTAGCATAGCAGCCCTGTCATAGGTAATCTCAGGTTCTAGCT 8765
 Qy 1634 TTACCCAGGAGTCTACGGCACCGTGTACACAGCATGAGATGATGATGTC 1693
 Db 8766 CTACTCC-GAGAGATTCAGGGACTGTCACTAATCTGATGATGGAGATCTGGCAT 8824
 Qy 1694 GCTTATGGATTCTCCGCTTAAAGGAAGATGTTCTGTGAGGAGATCTAACCA 1753
 Db 8825 CCTCAGGAAACTCTGCAAACTAAAGATGAGATGTTCTCCAAAGTGTGAACTG 8894
 Qy 1754 CTACACCACGAACTTCTGTCATCCATCTGTTGAGGAGATGAGATGGGCTGAC 1813
 Db 8885 CACACCTCTCTAATCTCTTCTGATCATCTGATGATGATGATGATGATGATG 8944
 Qy 1814 AACCGCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1873
 Db 8945 CAATACCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 9004
 Qy 1874 GAAAGTTGTTGAGCTTCGCTCAAGGAGATGGGTGAGCTGAGGAGGAGG 1933
 Db 9005 GATAGCTTGTGAGTCCCATCATTTCTGTTGAGCTGAGGAGGAGGAGGAGG 9064
 Qy 1934 TCACTGCGGAGTGTGAGTTCTGAGTTGACATGCTGAGGAGGAGCTTCACCCCTACAG 1993
 Db 9065 GCACCTAATGCTACTGGCAATTCTGGAGTTGAGCTGAGCTTCAACAGTT 9124
 Qy 1994 GTTCGAGCATGATGATGAGATGGCAACATGTTCTCCCTGAGTACGTACTAG 2053
 Db 9125 GTTGGAGACTCTATAGAGGAGGAGCTTCAAGCTGCTGAGGAGTACAGCA 9184
 Qy 2054 GATTCCTGAGGAGGAGGAGCTTCTGAGGAGGAGCTTCAAGCTGAGGAGG 2113
 Db 9185 GATAATGAGGAGGATACATGTTAGGCTCTGAGGAGGAGCTTCAAGCTGAGGAGG 9244
 Qy 2114 CAGTCGGCAACTGAGGAGTTAGTCACCGAGGAGCTACAAATAGAAGATGTTGATCA 2173
 Db 9245 CGTCGCCATTGAGGAGCTCTCTGAGAAGCT-----GCTTGGATG 9295
 Qy 2174 GACATATGATAGTAGGAGGAGGAGTTGACACGAGCATGATCATTCAGTGAGCATAT 2233

APPLICANT: Wright, David A.
; APPLICANT: Voytas, Daniel F.
; TITLE OF INVENTION: NUCLEIC ACIDS RELATED TO PLANT
; TITLE OF INVENTION: RETROELEMENTS
; FILE REFERENCE: 08411-031001
; CURRENT APPLICATION NUMBER: US/10/315,515
; CURRENT FILING DATE: 2002-12-10
; PRIORITY APPLICATION NUMBER: US 60/339,060
; PRIORITY FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 123
; LENGTH: 13868
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-315,515-123

Query Match 32.8%; Score 1025.4; DB 16; Length 13868;
Best Local Similarity 69.0%; Pred. No. 4.4e-274; Matches 1604; Conservative 0; Mismatches 606; Indels 115; Gaps 10;
Matches 1604; Conserved 0; Mismatches 606; Indels 115; Gaps 10;

QY 847 ACTPACATTAACGTTATCTTGTACTTGTTCTGTTTGTGTTCATCATGAGAAC 906
Db 8654 ACTAACTTATGACATTGACATTGACCTTGACGTTAGTCATAACCCCTACAGGAGAACTATGAGC 8713
QY 907 TACAGTGGAAATCTCTATGGACCCCTGATTAATCTGGTGAAGGTTAGTCCTGTTCAAGGAGAACTATGAGC 966
Db 8714 TACAGTGGCAGITCTTGTGTTGATCTCTGACTACACTGATGAGAAGAACTATGAGC 8773
QY 967 ACTAGACCGACTGAGAAGAACTGTTACAGGAGCTATGGGATGACGCTGC 9763
Db 8774 TCAAGCAGAGAGAGACAGAGAACTGTTACAGGAGCTATGGGATGACGCTGC 8814
QY 1027 GCAGCTGACGTAATCAGAGAGCTGAATCTGCTGGAGGAGGGCAGTCAGT 1086
Db 8815 -----AAGAAAGCTGAGATTCAGGAGAACTGTTACAGGAGCTATGGGATGACGCTGC 8857
QY 1087 AGATATGCTGATGAGGATATCAAACCTGAGTATGAGCTATGCCAGGTCTGG 1146
Db 8858 AGGTATGCTTATAGCAGAAGATGTTGGAGGCTACTCACCTGTTATGAGC 8917
QY 1147 GAGACGAGACTGACAAATCCGGAGGTTACAGTGGAGGAGPATATGAGCTT 1206
Db 8918 GCTTACCAACTCTGCACGCCGAGATACTGGCTACTGAGGAATATGGCAAG 8977
QY 1207 GAGATGATGACTCTGGGAAGAGGTTCTGTGATGAGCTTAGCCAGTGG 1266
Db 8978 AAGCTGATGAGCTCTGTGACCAAGTGGAGGCTACTGACACAATCGGA 9037
QY 1267 TTAATGGAGGAGCTGCAGCATGTGAGGAGGTCTGTTGCTGACACTTGTG 1308
Db 9038 TTGTGAGAGATGTTGCGACCTGTGACCAAGTGTGATCTGAGACCTTGTG 9097
QY 1309 -----ATAGGAGGAGPATACGAGTTCTTCCACATGCAAGTGGAAATG 1355
Db 9098 CGTATGATGAGCATATGAGAGACATACATCTTCACACGCAAGTAACCTC 9157
QY 1356 TATGAGGAGCTACAGACTGAGCTTGAGCTGAGTACCATGGGTAGGCTCTGACGTTCTTA 1415
Db 9158 TACCAAGTGTGACCTGAGTTGAGTGTGAGTGTGAGTGTGAGGTTGGATCTCC 9217
QY 1416 GTGGATGACAGGGTACAGGTTAGATGAGAAATTGGAGAAGACTGTTGGTCCCT 1475
Db 9218 GTGCATGTCATGAGTCAGGTTACATCATCAGGGATGTTGGGATCTCC 9277
QY 1476 AGTGGAAAGGAAACCCAGGTGAGGGAGGCTAAGGATTGGGCTACT 1535
Db 9278 AGTGGAAAGGGATCTAGCCAAAGTGAAGAGAA-----GACTTGTGATCACC 9328
QY 1536 ATGGGAACTACGGCTAACTGGCGGGTCAAGGCAACCAATCGGGTCT 1595
Db 9329 ATGGGAGCTCGTGTGATCTCCAGGTCAGGCAACTGAGAACGCGCTC 9388
; GENERAL INFORMATION:
RESULT 7
US-10-315-515-123
; Sequence 123, Application US/10315515
; Publication No. US2003016619A1
; GENERAL INFORMATION:

Qy 1596 GTGAGTGCCTACTTCAGCCTCGGGTGCATGTTTACTCCAGGGGTACAGC 1655
Db 9389 GTCACAGGAGTCTCCAGGCTCTGAGCACTTGCTGAGCT 9448
Qy 1656 ACGGTCTAACACAGACATAGATGATGATTAGGGTTAGGGATTCGCC 1715
Db 9449 ACTGTAACCTCTGATAGAGATGATGCAATGCCCTCAAGGA 9508
Qy 1716 ACAAAAGAAGAATGCTCTAGAGAGATTTAACGACTACCCAGTATGCTG 1775
Db 9509 ACTAAATAATGCCATGCCCTCAGGTTAACCTAACACCTCTACTCT 9568
Qy 1776 TTGATCCATCTGTGGGTTAGTAGTGCAGCTGACAACGGGAGAGTA 1835
Db 9569 CTGATCCTCTGTGGTGGATACAAAGCTGGGGTCAGCAATACCGCA 9628
Qy 1836 GGAGACTATCGTGGGGTTGACGGCAATCTGAAGTTGGGGTGC 1895
Db 9629 GGGCTCTGATAGTGGGTTGACACGATCTGATAGCTGTGGTCCACTC 9688
Qy 1896 AAGGAAGTAGGGTTAGCACCGAGAATGATGACTTGCTTGGCCGATG 1955
Db 9689 ATTCCTGCTGGACTCGAGCCGGTGGACATGGATATGGACACTGCA 9748
Qy 1956 TCTGAGTTTACATGTTGGGACTTTCAAGCTGAGCTCATGTTAGA 2015
Db 9749 CTGGACTTGTGATGGTGGAGATTCACGGTCACTGGACTCTAGCAG 9808
Qy 2016 ATCGCCAAACATCTTCCCCGATTACCTACTAGGATCTCGAGGGAGAC 2075
Db 9809 AGAGCTAACATCCTCTCCGATGCCGATCTGAGAAATGAGTACATT 9868
Qy 2076 GACTCAAGCTGCGCTTGAAGATCTTATTGAGGGCACTCCGGCAACT 2135
Db 9869 GATTTAGCTGAGCTGAGATTTGGATCTACATGAGAACGCTCACC 9928
Qy 2136 AGTCACACCGAGGGACTACATAGAGATGTGGAGAGATATGATGGGG 2195
Db 9929 GATCTCTGTGAGACT-----GCTTGGATGGGATGAGATAGGGG 9979
Qy 2196 GAGTTGACAGGAGGCTATCATTCAGGGATATACTCCAGGAGAAANGC 2255
Db 9980 AGTTGACACTAGCATGATGACTTGTGTCACAGTACTCCAGGAGCA 10039
Qy 2256 AGTTGAGCAGCTCACAGGAAACACAGCAGCTGAGGGTGAAGAACAGG 2315
Db 10040 AGCTGACTGAGCTGATAGATAACAGTAATTCAGAATGGCAGAGGAGAC 10099
Qy 2316 AGTTTACTGCGCAAGGCTCAGGGTATCAGTTCTGAGGACAGATGCG 2375
Db 10100 AGCTGATCTGGCAAGT-----TTCACTCTGTGAGATAGCTGCT 10150
Qy 2376 TCTTCCTACTGAACTATCCCAATGACAGGTCCTCAGGACATGCTGGAGGAT 2435
Db 10151 TCCTCCACCACTGCTATTCCACAGGTTCCCTGGAGATSCATCGAGGATT 10210
Qy 2436 GACGCC-----GACCTAGAGAGAGATCTGAGTCTGGAGG 2483
Db 10211 ATGAAACCGGCACAGACCTTGGAGACAGAGAGAGGCTACAGCTCAGG 10270
Qy 2484 CATTCACTCATCGAGGCTCTGAACTTAGGAGAATGGGACTACTGATC 2543
Db 10271 ATTCGTCATTGAACTCCGGACACAGAGAGAGGCTACAGCTCAGG 10330
Qy 2544 AGCAGGAGGAGGAGGACTCTCGAGCTCTGAGTTACCGACGCCGCTGCC 2603
Db 10331 AGCAGC---AGTACAGCCTATTCACTCGAGGAGATCACTCGACGCCGCTGCC 10387
Qy 2604 ATAGAGAAGAGAGGAGGTTGAGTCTCTGAGGGCTCTGCCGACAGAGCTGATGAG 2663
Db 10388 AGCAGAAGGAGAGGAGGCTGAGGTTCCCTCAGGGGCTGCCGACAGAGCTGATGAG 10447
Qy 2664 ATCGAGTACCCACATGCTGGAGCTGATACGGAAACATGCGGGTCGCTATGGCTTGGAG 2723

RESULT 8
US-09-965-553-24
; Sequence 24, Application US/09965553
; Patent No. US2000112259A1
; GENERAL INFORMATION:
; APPLICANT: Wright, David A.
; ATTORNEY OR AGENT: Voyas, Daniel F.
; TITLE OF INVENTION: Plant Retrolelements and Methods Related Thereto
; FILING REFERENCE: P-105 ISURF Plant Retrolelement
; CURRENT APPLICATION NUMBER: US/09/965,553
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/322,478
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087125
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 24
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-965-553-24
Query Match 24.1%; Score 751.6; DB 9; Length 1857;
Best Local Similarity 65.3%; Pred. No. 3.3e-198; Matches 1250; Conservative 0; Mismatches 564; Indels 100; Gaps 6;
Matches 1250; Conservative 0; Mismatches 564; Indels 100; Gaps 6;
Qy 898 ATGAGTAACTACAGTGGAAATCCCTCTGACCCGTGATATAATGGGATGAGCTAG 957
Db 1 ATGAGCAATTACAGCAGCTCTGTTGATCTGAGCTACATGAGCTAG 957
Qy 958 TCTGCTTCACTGAGGGTGGAGAGACATGTTAGGAGCTATAGGATGATTT 1017
Db 61 TGTGCACTTCAAGGCCAGAGAGACAGAGAGATGAGCTAG 110
Qy 1018 GAACTCTGAGCTGAGCTAATCAAGAGAGCTGAAATCGTAGGAGAAGGGCG 1077
Db 111 -----AAGGAAAGTGGAGATAGCCGAGGAAAGGAGCG 144
Qy 1078 ATGCGAGTATGAGCTGATGAGGATATCAAATGAGTATGAGGAGAGCTA 1137

Db	145 ATGGAGAGGAGGATGACCTATAGACGAGATCTGGAGGAGGATCATGCCAGACAG	204	QY	2187 GATCAGGGGAGTTGACGAGCATATTCAGGATATCCAGCAG 2246	
Qy	1138 TSGCGCAAGGAGAGGAAGCTACTGACACAAATCTGCAGGAGGTACAGTGGAGGATATC	1197	Db	1276 GGAGCAAGTAAGTCGACACTGATGATCATCTTGACATGACATCTCCAGGAGG 1335	
Db	205 ACTCGCAGAGCTACCAAACCTCTGCACAGCCGACATATTGCTGCGAGAATGTT	264	Qy	2247 AAAGCAGAGGTTGAGCAGGCTCACAGGAACACIGCAAGCTGCGAGTGGTGCAG 2306	
Qy	1198 AGATTCITGAGTAGAATGACTCTGGAGAACAGGATTCCTGATATGAGCTTACCC	1257	Db	1336 CAGGCAGAGCTGAGCTGAAGTCATAAGAATTACAGTAATGCGAGAGTGTGCGAG 1395	
Db	265 AGGCTTTCAGCTGAACTGAGTGTCTGAGCAGGATATCTCTGACTCTACATGCA	324	Qy	2307 AACAGAGTAAGTACTTGCCCAAGTGTGCTCAGGCTATCAAGTTGAGAACATTC	2366
Qy	1258 CAGTTGGGTACTGGAGGAGGAGTGGAGATCTGAGAAGTGTGAGAAGTGTGATCTG	1308	Db	1396 AACAGAGCAGGTGATGCCAAGT 1446	
Db	325 CACTCGGATGTTGGAGATGTCAGGACCTGTCACCAAGAGTGTCACTGGACATTTG	384	Qy	2367 AGCTGCTCTCTCCACTACAACATTCGGCATGAGCTGAGCTCCCTCGAGCACATGCCCTCG 2426	
Qy	1309 -----ATAAGGAGGAGCAATCGAGTTCTTCACACTSAA	1346	Db	1447 AGTGTCTTCCCTCCACACTGCTATTCACAGGTAACCTCTGATCGCTACATCG 1506	
Db	385 ATGGCTTATCCGTATGAGGATAGAGAATGAGAGAATACATTCCTCCACACTCAA	444	Qy	2427 AGGRAGATGACCC-----G3CCGAGCTTACAGGATGAGAGATCTGAGCAGCTC 2474	
Qy	1347 GTGGAATGATGAGGAGGACTCACAGACTTGACGCTGAGCTGAGTGGTTAGCTCTG	1406	Db	1507 AGGAGATAATGACCTGCGACAGSCTGACTGAGAGAGATTCAGGAGAATGCCCACATTC 1566	
Db	445 GTGAGGCTCTACCGAGGATGACTCTGAGTGGATGAGGTTGGATCTGAGCTCTG	504	Qy	2475 CCTCGGGGAGCATCATTCATCGAGCTGAGTGGAGTGAAGGATGGAGACTCTC 2534	
Qy	1407 ACGTCTCTAGGGATGAAGCAGCGTACACAGATTAGTCAAGAAATTGAGAAGACTGTT	1466	Db	1557 CAGCAGACAGGTGATGCCAAGT 1626	
Db	505 CGATTTCTGTTGATGGTCATGAGTACAGGTTACATCAAGCAGTGGAGATGTT	564	Qy	2535 ACTCGATCTAGCAGCAGAGCACGACTCTCGCAGCTCGTAGTTAOGCGAACCGGT 2594	
Qy	1467 GGTTCCTCTAGTGGAAAGGGAAACCCACCGTTGAGGAGACTTAAGGATGTT	1526	Db	1627 ACTCGATCTAGCAGC-----AGATCACGCTCATCACGAGGATACTCGACCGGT 1683	
Db	565 GATTTTCCCGATGAGAACCGGATCTGGCAAGAATGAGAAGACTG	624	Qy	2535 GCTCGCCCAATGAGAGAGAGGGTCACTGAGACACAGAACAGAACAGCTC 2654	
Qy	1527 TGGCTACTATGGGAAACATCTACCGCTAACTCGACCCGGTCAAGAGAACAAATC	1586	Db	1684 GCTCGCCCAAGCAGAGAGAGAGGGTCACTGAGACACAGAACAGAACAGCTC 1743	
Db	625 TGCATCACCATCGCAGCTGTAACGGCTCAAGAAGAAGCTA	684	Qy	2655 GCTCGATGAGATCGATGCCACATCGCAGGAGTATGGAGCATGGGGTGTCTG 2714	
Qy	1587 CGGAGTCTCTGTAATGCTGACTTTCAGGGCTCGTGTGCAATGTTTATCCAGGGAG	1646	Db	1744 GCTGATGAGGCTGAGTACCCATCTGCTGAGCTGATGAGACAGAACAGAGGTTCTG 1803	
Db	685 CGCAGCCCTGTCATCAGGACTCTCCAGGTTCTGAGTGGATGATCTGAGCTCTA	744	Qy	2715 GCTGGGAGCAATCACAGCAGGCAATGACTACCAACCTCGTCATATTGAC 2168	
Qy	1647 TCTACAGGCCACCTGTCAPACAGACATGAGATGATCTGAGCTTATGGATT	1706	Db	1804 GCCTGGAGCAATGCCAGGCAACCATGAGGAGCAACTAGTCATCTCGAC 1857	
Db	745 ATTACAGGGACTGTCACACTCTGATGAGGATGAGATCTGAGGAGACT	804			
Qy	1707 CTGGCCCTAACAAAGGAGAATGTCCTGAGGAGATCTAACGACTCACCACAGA	1766		RESULT 9	
Db	805 CTCCGCCAACATAAAAATGGCTGTCCTCAGGGTGAAGTCACCTCTCT	864		US-10-615-005-24	
Qy	1767 ATGGCTCTCTGATGTCATCTGTCGGTGGATGAGTGGCTGACAAACGGCAAGAG	1826		; Sequence 24, Application US/10615005	
Db	865 ATACTCTCTGATCATCTGTCGGTGGATACAAACCTGGGGTCAGCAATACCGCAAG	924		; Publication No. US20040016018A1	
Qy	1827 AAGCTAAGGAGGACCACTATGGCTGGTGGCTGAGGCAATTCTGAAAGTTGGA	1886		; GENERAL INFORMATION:	
Db	925 AGAGCACGAGGACCTCTGAGCATAGGTTGGCTGAGCAACTTCTGATAGCTG	984		; APPLICANT: Wright, David A.	
Qy	1887 GTTCGGCTCAGGAGGAGCTGGTGGACCGAGAATGATGCGCTGCTGGCGGA	1946		; APPLICANT: Vytas, Daniel F.	
Db	985 GTGCCCACTCTGATGTCGGCTGAGGCACTTCTGAAAGTTGGA	1044		; TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto	
Qy	1947 GTGAGTCTCTGAGGTTGACATGGTGGACGACTTCACGGCTACAGGTTGAGCT	2006		; FILE REFERENCE: P-1065 ISURF Plant Retroelement	
Db	1045 TGCCAATTCTGGAGTTCAATGAGTTCACAGGTCACTCT	1104		; CURRENT APPLICATION NUMBER: US/10/615-005	
Qy	2007 TCGATGAGATGTCGCAACATCTCTTCCCTGATTACGGCTACAGGATCTGAGG	2066		; CURRENT FILING DATE: 2003-07-08	
Db	1105 ACAGACAGGGAGGCTAACATCTCTCCCTAGGCCCTGAGGTCACAGGATAATCGAGG	1164		; PRIOR APPLICATION NUMBER: US/09/322,478	
Qy	2067 AGGACATCTGACTCAACCTGGCTTGGAGCTTATTCAGGGAGTCGCCACT	2126		; PRIOR FILING DATE: 1999-05-28	
Db	1165 GATGACATGATTAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTCAGGATTA	1224		; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/087125	
Qy	2127 GAGGAGATTGTCACCGAGGAGCTAGATAGAGATGTTGAGAGACATGATA	2186		; NUMBER OF SEQ ID NOS: 41	
Db	1225 GATGAGGAGGAGCTCTCTGAGAGACT-----GCTCGGATGGATGAGAT	1275		; SOFTWARE: Patentin Ver. 2.0	
				; SEQ ID NO: 24	
				; LENGTH: 1857	
				; TYPE: DNA	
				; ORGANISM: Arabidopsis thaliana	
				US-10-615-005-24	
				Query Match 24.1%; Score 751.6; DB 17; Length 1857;	
				Best Local Similarity 65.3%; Pred. No. 3_3e-188; Matches 1250; Conservative 0; Mismatches 564; Indels 100; Gaps 6;	
				Qy 898 ATGAGTAACATGCTGAAATCTCTGAGGCTTATATGAGGATGAGCTTAAAG 957	
				Db 1 ATGAGCAATACGGCTGCTCTCTGAGCTACACAGCATGAGACAGCA 60	

Qy 958 TCTCTGTTCCACTAGACGGGAGTGAGGAGCAGATGTTACAGGAGCTATGGATTTAGGATTT 1017
 Db 61 TCGTCATCTTCAGGCCAGAGCACAGAGAACATAAGAAAGTTCAG----- 110
 Qy 1018 GAACTGCTGAGCTGAGTATCAAGAAGAGCTGAATGGTAGAGGAGAGGGG 1077
 Db 111 -----AAGGAAGCTGAGATAAGCCGAGGAGAGGG 144
 Qy 1078 ATGTCGAGTAGATAGAGCTGATTGTAGGAGATTAACAGTGGATGAGGAGTCAG----- 1137
 Db 145 ATGAGAGAGAGGATGAGCTTAGAGGAGAGGAGCTGAGACAG 204
 Qy 1138 TGGCGCAGGAGACAGAGCTCTGACAATCCGAGGAGGTACAGTGAGGAGRATAC 1197
 Db 205 ACTCGCAGAGCTTACCAACTTGTGCAACAGCCGACATATGGAGGAGGAG 264
 Qy 1198 AGATCTTGGAGATGAGTACTCTGGAGAACAGGAGTATCTGATATGAGACTTAGCC 1257
 Db 265 AGGCTTTCAAGCTGATGAGTGTAGCTGAGCTGAGGAGTATCTTGCTGACCTCACITGCA 324
 Qy 1258 CAGTGGGGTACTGGAGGACGTGAGCATGTTGAGAAGTGTACITG----- 1308
 Db 325 CAACTGGATTTGGAGAGATTCAGGACCTGAGACTTGACACTTG 384
 Qy 1309 -----ATAAGGAGGAGACATGAGTTTCAACTGCAA 1346
 Db 385 ATGGCTTATCGTAGTGTAGCATATGAGAGATGACATACATCTCCACACTACAA 444
 Qy 1347 GTGGAATGTTGAGGACTCACAGCTTGGTGTGATACATGGGTGTTGGCTCTG 1406
 Db 445 GTGAGAGCTCTAACAAAGTATGACCTCTGATAGTGGATTGAGGATGGATCTG 504
 Qy 1407 AGTCTCTAGTGGATGACAGGGTACAGATTAGATCAGAAATTGAGAAGCTGTT 1466
 Db 505 CGATTCTGTGATGTCATGAGTCAATCAGGATGTTACATCAGGATGAGGATCTT 564
 Qy 1467 AGTTTCTCTGGAAAGGGACCAACCCCAGTTGACAGGAAAGCTTAAAGGTT 1526
 Db 565 GATTTCTCACTAACAAAGTATGAAAGGAGGTTAAAGGAGGTTAAAGGTT 624
 Qy 1527 TGGCTACTATGGAAACAATCTACCTAACTGAGCTTCAAGGAAAGGAAACCAAC 1586
 Db 625 TGGATCACCATTGGAACTCTTACCTGAACTGCTTCAAGGAAAGGAAATCAGATA 684
 Qy 1587 CGAGACTCTGATCTCTACTTCAAGGCTGGTCCAAAGTTTACTCCAGGG 1646
 Db 685 CGCAGCCCTGTCATCAGGTTCTCAGGTTCTGAGCAAGTACTCTCCGGAG 744
 Qy 1647 TCTACAGGCACGGTGTAAACAGACATGAGATGAGATGAGTCAAGGCTTATGGATT 1706
 Db 745 ATTACAGGGACTCTGTCACTCTGTGATGAGATGAGTCAATGGCCCTAAAGGAAT 804
 Qy 1707 CTCCGCTTACAAAGGAAGATGTCCTGAGGAGGATCTAACGACTCCACCGATA 1766
 Db 805 CTCGGCCAACAAATAATGGCATGTCCTCAGGTGAAGTCATGACACCTCTCT 864
 Qy 1767 ATGCCCTGTTGATCCCTCTGGTGGTACATGAACTGGGGCTGACAACGGCAAGAG 1826
 Db 865 ATACTCTCTGATCCATCTGTGATGAACTAACAAACTGGGGTCACAAACCGAAG 924
 Qy 1827 AAGGTAAAGAGGAGCAATGAGGGTGTGGGGCTGAGGAGCTTGTGAGA 1886
 Db 925 AGAGCAGCAGGCCCTGTGAGTGGGGCTGAGGAGCTTGTGAGA 984
 Qy 1887 GTTCGGCTCAAGGAACCTGGGTAGACCGAGATGAGTGTGATGCTACCTGGCA 1946
 Db 985 GTCGGCTCAAGGAACCTGGGTAGACCGAGATGAGTGTGATGCTACCTGGCA 1044
 Qy 1947 TGTGAGTCTCTGAGTTGACATGGTGGACTTCAACGGTTCAGGTTGAGCATCA 2006
 Db 1045 TCCAAATCTGAGGTTGACATGGTGGACTTCAACGGTTCAGGTTGAGCATCA 1104
 Qy 2007 TCGATTAGAACTGCCAACATCTTCCCTCATTAAGCTACTAGGATCTCGAGGG 2066

RESULT 10
 US-10-395-607-24

; Sequence 24, Application US10395607
 ; Publication No. US20040019328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wright, David A.
 ; APPLICANT: Vojtas, Daniel F.
 ; TITLE OF INVENTION: Plant Retroelements and Methods Related
 ; TITLE OF INVENTION: Threto
 ; FILE REFERENCE: 08411036001
 ; CURRENT APPLICATION NUMBER: US10/395,607
 ; CURRENT FILING DATE: 2003-03-24
 ; PRIOR APPLICATION NUMBER: 09/586,106
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: 09/322,478
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/087,125
 ; PRIOR FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 24

; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-395-607-24

Query Match 24.1%; Score 751.6; DB 17; Length 1857;
Best Local Similarity 65.3%; Pred. No. 3 3e-198; Mismatches 564; Indels 100; Gaps 6;
Matches 1250; Conservative 0; Mismatches 564; Indels 100; Gaps 6;

Qy 898 ATGAGACTACTGTGAAATCCTCTATGCCCTGATTATATGCGTGGAGCTAG 957
Db 1 ATGAGACTACTGTGAAATCCTCTATGCCCTGATTATATGCGTGGAGCTAG 60

Qy 958 TCTGGTCCAATGACCGGAGTGGAGAGCACTGTTACGGAGCTATAGGAATT 1017
Db 61 TCTCATCTTCAAGGCCAGAGAGAACAGAGAACAGAGAACAGAGAACAGAGA 110

Qy 1018 GAAAGCTCTGCAAGCTCGAGTCAGTCAAGAGAGAGCTGAAATGCTAGAGGAAAGAGGGCG 1077
Db 111 -----NAAGGAAAGCTGAGATAGCCGGAGAGAGAG 144

Qy 1078 ATGCGAGTAGATATGAGCTGATGAGGAGATAAACAGAGTATGAGCAGACTCA 1137
Db 145 ATGAGAGAGAGGATATGAGCTGATGAGGAGATAAACAGAGTATGAGCAGACTCA 204

Qy 1138 TGGCGMAGGAGAGAGAGCTGACAAATCGACAGGTTACAGGGAGGATATC 1197
Db 205 ACTCGAGAGCTTACAAACTCTGCACAGCCGACATATTCCTGCTGAGGATATT 264

Qy 1198 AGATTCUTTGAGATGAATGATGAGCTGAGGAGGATTCCTGATATGAGCTTAVGC 1257
Db 265 ACGCTTTCAAGCTGAAATGAGTCTGAGGAGGATTCCTGATATGAGCTTAVGC 324

Qy 1258 CAGTGGGGTACTGGAGGAGCTGAGGAGGATTCCTGATATGAGCTTAVGC 1308
Db 325 CAACTCGATGTTGGAGAGTGTCACTGACAAATGAGCTTAVGC 384

Qy 1309 -----ATAAGGAGAGACAATCGAGTTCTTCACACTGCAA 1346
Db 385 ATGCCTTATCGTATGAGATGAGAGACAATACAAATCCCTCACACTCAA 444

Qy 1347 GTGGAATGTGAGGAGCTACAGACITTGAGCTGATACATGGGTTAGCTTGT 1406
Db 445 GTGAGCTTACCAAGGTATGACCTCTGATGAGTTGGATTGGATCTG 504

Qy 1407 ACCTCTTGTGAGACAGCGCTTACAGATTAGTACAGAAATGGAGACTGTT 1466
Db 505 GCAATTCTGTGATGAGCTTACAGATTAGTACAGAAATGGAGACTGTT 564

Qy 1467 GGTTCCCTAAGGAAAGGAAACCCGTTGACAGGGAGGCTTAAAGTTTG 1526
Db 565 GATTCCTCAGTGAACCGGATCTAAGCAAGATGAGAGAGAGTGAAGCTG 624

Qy 1527 TGGCTACTATGGACAACTTACCGCTAACTCGAGGCTTACAGAGAACATC 1586
Db 625 TGGATCACCATTGGCAGCTGTTACGGTGTGAGCTTCCAGGTCAGATCGATA 684

Qy 1587 CGAGCTCTGTTGAGTGCCTCTTCAGGCCCTGGCTCACTTTCAGGGAG 1646
Db 685 CGCAGCCCTGTCATCGATCTTCAGGCTTACAGGCTTACAGGAGAG 744

Qy 1647 TCTACAGGCCACCTGTCTAACACAGACATGAGATGATGAGATGAGATGATC 1706
Db 745 ATTACAGGGACTCACTGATGAGATGATCAGTCAAGGAGGAG 804

Qy 1707 CTTCGCCCTTAACAGGAAAGATGTCCTGAGGAGATCTGAGCTTACAGGCTTACAGGAG 1766
Db 805 CTTCGCCAACTAAATGGCATGTCCTCAGGGTGAAGTCAATGAGACACCTCTCT 864

Qy 1767 ATGCTCTGTTGATCCATCTGTGGTACATGAGCTGGCTGACAAACGGCAAGAG 1826
Db 865 ATRACTCTCTGTCATCCATCTGTGGTGGATACAAACCTGGGCGTCAACATACCGAG 924

Qy 1827 ATGGTAGAGGGCACTATGCTGGTGGCGTGTGAGGCCAATCTGAAAGTTGGGA 1886
Db 925 AGAGCAGGGCTCTGTGATAGGCGTGTGAGACCTTATTCGATAGCTGTGGA 984

Qy 1887 GTTCGGCTCAAGGAGTAGGGTTAGCAGGAGATGAGCTGATGACTCTGGCGGA 1946
Db 985 GTCCCATTCATCTGTGGATGAGTCAAGGAGCACTGAGATGAGCTGAGCTACTGCGC 1044

Qy 1045 TGCCAACTCTGGAGTTGCAATGGTGAAGCTTCCAGGTCAAGGTCACTGAGACTCT 1104

Qy 2007 TCGATTGAACTGCCACATCTTCCCCTCATTTACGGTACTAGATCTCGGGC 2066
Db 1105 ACAGACAGGAGGAGCTAACTCCATCCCTCTCCTAGCCCTTGGTCAACCGGATAATCGAGGGA 1164

Qy 2067 AGAACACTGACTCAAGCTGGCTTGAAGATCTTATTGGAGGGAGTCCGCAACT 2126
Db 1165 GATAACATTTGATTTAGGCTTGGAGATGGACCCCTACTATGAGAACGCTTCCACCTT 1224

Qy 2127 GAGGAGTTAGTCACACGGAAGGCTACAAATGAGAGATGTTGAGACATATGATA 2186
Db 1225 GATGAGAGCATCTCTGAGAAGCT-----GCTCGATGGATGGATGAGAT 1275

Qy 2187 GATGAGCGGAGTTGACAGGAGTATCATTTCTGAGCATATACCTCAGGGAGG 2246
Db 1276 GAGGAGCTTAAAGTCTGCAACTGACATGACATGATCTACTTCTGACATGACCTTCAGGG 1335

Qy 2247 AAAAGCAGAGTTGACCGAAGGCTCACAGGAACTGAGAACGCTGAGAAGTGGTGAAG 2306
Db 1336 CAGAGCAGAGTTGACTGAACTCATAGGATTTAGTAAATGGAGAGCTTCA 1395

Qy 2367 AGCTGCCTCTCCACTACAACTATTCCGAATGAGCTCCTCGAGACATGCTCG 2426
Db 1447 ATGTCCTTCCACACTGCTTACCTATTCCACAGGTACAACTCTTCAAGGATGCTCG 1506

Qy 1396 AACGAGCACAGGCTGATGCGCACTG-----TTCAAGCTTCTGACAGAACCTG 1446

Qy 2427 AGGAGATGAGCC-----GCCCGAGCTTGAAGAGCAGAGAATCTGATGTC 2474
Db 1507 AGGAGATAATCCACCTGGCACAGGCTTGAAGCTTGAAGAGGTTCCACATG 1566

Qy 2475 CCTCGGAGGCACTCATCTTCAGGCTCTGGAGAATAGGAGAACGACTCT 2534
Db 1567 CAGGCTAGCATCTGTCATTCGAATCCGGGAACACAGAGAGAGGCTTACACTC 1626

Qy 2535 ACTCGATCTGAGCAGGAGGAGGAGCTCTGGAGAATAGGAGAACGACTCT 2594
Db 1527 ATGCGACTTACAGC-----AGTACACGCTCATCTGAGCTGAGCTGACCGGGT 1683

Qy 2595 GCTGGCCGAATAGAGAGAGAGGAGTGGAGTACCTCTGAGGGGTGGGGCCACAGA 2654
Db 1684 GCTGGCCGAAGGAGGAGGAGATGTCAGTTCTCTGAGGCGTGTGGCCCAAGA 1743

Qy 2655 GCTGATGAGTGTGAGTCACTCTGCTGAGCTGAGCTGAGCTGAGCTGACCGGGT 2714
Db 1744 GCTGATGAGTGTGAGTCACTCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1803

Qy 2715 GCTTGGAGGAACTACAGGGAGGCCATTGACTACCAACTCTGCTCATTTGAC 2768
Db 1804 GCCTGGAGCAATCGCAGGAGCCATTGACTACCAACTCTGCTCATTTGAC 1857

RESULT 11
US-10-799-670-24
; Sequence 24, Application US/10799870
; Publication No. US2004015888A1
; GENERAL INFORMATION:
; APPLICANT: Wright, David A.
; TITLE OF INVENTION: PLANT RETROELEMENTS AND METHODS RELATED THERETO

; FILE REFERENCE: P-1055A
; CURRENT APPLICATION NUMBER: US/10/799, 870
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/586, 106
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/087, 125
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/322, 478
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 24
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-799-870-24

Query Match 24.1%; Score 751.6; DB 19; Length 1857;
Best Local Similarity 65.3%; Pred. No. 3.3e-198;
Matches 1250; Conservative 0; Mismatches 564; Indels 100; Gaps 6;
Qy 898 ATGAGTAACTACTAGCGAAATTCCTTATGACCCCTGATTAACTGGATGAGCTAAG 957
Db 1 ATGAGCAATACAGTGCGACTCTCTGTTCTGTTCTGACTACATCGATGAGAGAA 60
Qy 958 TCTGTGTCACCTAGACCGGAGTGAGCAGATTTACGAGCTATGGATGAGCTAAG 957
Db 61 TCGTCATCTTCAGSCCGAGAGACAGAGAAATCGAAGTTCAG----- 110
Qy 1018 AACGCCTCTGAGCTGAGCTGACGTAATCAAAGAAGAGCTGAATTCGCTAGAGGGCG 1077
Db 111 -----AAGGAAGCTGAGTAGCCGAGGAAGAGCG 144
Qy 1078 ATGTCGAGTAACTATGAGCTATGAGATACTAACATGAGCTATGAGCAAGTCA 1137
Db 145 ATGAGAGAGAGCTATGAGCTATGAGCTATGAGAGCTGAGGAGGAGPACATCCTGACAG 204
Qy 1138 TGGCGCAAGGAGAGCTCTGACAACATCGACGAGGTTACAGTGGAGGAGTATC 1197
Db 205 ACTCGCGAGCTACCAACTTGTGACAAGGCCGACATATTCGCTGAGGATATGTT 264
Qy 1198 AGATCTTGTGAGTGAATGACTCTGGGAAAGGAGTATCCCTGATATGAGCTTAGCC 1257
Db 265 AGGCTTTCAAGCTGAACTGAGCTCTGAGCTGAGGATTCCTGACGACTCAGTGCA 324
Qy 1258 CAGTGGGTACTGGGAGGACTGAGCATCTGTTGAGAAGTGTCTG----- 1308
Db 325 CAACTCGATTTGGAGATTCACCACTGTGACCAAASTGTCATCTGACACTTG 384
Qy 1309 -----ATAAGGAGGAGACAATCGAGTTCTTCCACATCGAA 1346
Db 385 ATGGCTTATCCCTATGAGATGAGAGACATACATTCCTCCACACTACAA 444
Qy 1347 GTGGAATGTAGGAGCTACAGACTTGAGTGTGATGAGATGGATCTG 1406
Db 445 GTGAGGCTTCAACGAGTACCTCTGATGAGTGTGAGATGGATCTG 504
Qy 1407 ACGTTCTTAGTGTGAGACACCGGTACCGAGTTAGTCAAGAAATGGAGAAGCTGTT 1466
Db 505 CGATTTCTGTGATGTCAGTACAGGATTCATCAACGATGGAGATGTT 564
Qy 1467 GGTTCCTAATGGAAGGGACCAACCCCGTTGACAGGAAGAGCTTGGATTG 1526
Db 565 GATTTCTCAGGAGCTAAGCCAAAGTGTGAGATGGCTGAGCT 624
Qy 1527 TGGCTACTATGGAACATCTACCGCTAACTCGAGCCGCTCCAGGAAACATC 1586
Db 625 TGGATCACCACTGGCACCTCTGACCGCTGAGCTGAGCTGAGCT 684
Qy 1587 CGAGCTCTGTGATTCCTACAGCTCGCTGGTCAAGCTGTTTACTCCAGGGAG 1646
Db 685 CGACGCCCTGTCATCAGGACTCTCCAGGTTCTGAGCCAAGTCACTGCCCAGAG 744
Qy 1827 AAGGTTAGGAGGACTATGGGTAGCAGGAGATGAGGAGCTGGATGAGCTGG 1886
Db 925 AGAGCACCGGGCTCTGTCATAGGIGGCGTGGAGACCTATCTGAGA 984
Qy 1887 GTTCGCTCAGGAGTAGGTTAGCAGGAGATGAGGAGCTGGATGAGCTGG 1946
Db 985 GTCCCACTCTAATTCGCTGACTCGAGCCAGAGCAATGGATATCGAGCAC 1044
Qy 1947 TGTGAGTCTCTGAGTTGACATGGTGGGACTTCACGGCTACAGGTTGAGATTCA 2006
Db 1045 TGCCATCTGAGCTTGAATGGTACAGTTCCAGGTTCACTGAGACTCT 1104
Qy 2007 TCGATTTAGATGCGAACATCTGTTCCCTGCTACTAGGATTCTGGAGGC 2066
Db 1105 ACAGAGGAGGAGCTACATCTCTCTCTAGCCCTGAGGTCACAGGATAATCGAGGA 1164
Qy 2067 AGGACATCTGACTCTGAGCTGCTGCTGGAGATCTTATTGAGGGCGTCCCAACT 2126
Db 1165 GATAACATGATTTAGGCTGAGATTGGAGCCCTACTATGAGAACTGCTCACCATA 1224
Qy 2127 GAGGAGATGTCACCGAGGAGCTACATAGAGAGCTTGTGAGACATGATA 2186
Db 1225 GATGAGGACGATCTCTGAGAGCT-----GCTTGAGATGGAGAAT 1275
Qy 2187 GATGAGGGAGGTTGAGCAGAGCTATGAGCTGAGCTGAGCTACCTCCAGGAGG 2246
Db 1276 GGAGCAGTAAGTTCGACACTAGCTGATGATCTGTCAGTACATGACTCCAGGAGG 1335
Qy 2247 AAACAGGAGTTGAGCTGAGGCTCACAGAACAGAGCTGAGCTGAGGAGATGTC 2306
Db 1336 CAGAGCAGAGCTGAGCTACATGAGCTAATGAGAATTGAGCTGAGGAGAAG 1395
Qy 2307 AAACAGGAGTTGAGCTGAGGCTCACAGAACAGAGCTGAGCTGAGGAGATGTC 2366
Db 1396 AAGCAGGACAGGCTGATCSCCAAGT-----TTCRAGCTCTGAGACAGAGCTG 1446
Qy 2367 AGCTGCTCTCTTCACTACACTTCCACATGAGCTCCCTGAGCATGCTCG 2426
Db 1447 ATGTCGCTCTCTCCACACTGCTTCCAGGTTACACTCTCTATGGAATGCTCG 1505
Qy 2427 AGGAGATAGCCTGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2474
Db 1507 AGGAGATATGACCTGCGCACAGCTGAGCTTGGAGAGAGGAGGAGGAGGAG 1566
Qy 2475 CCTGCGGGCATCTCATCGAGCTCTGAGCTTGGAGAGATGGAGAAGACACTC 2534
Db 1567 CAGGCTAGGATTCGCACTGCAAGCTCGGAACACAGAGAGGAGGAGGAGGAG 1626
Qy 2535 ACTCGAGCTAGCAGGAGGAGGAGCTGAGCTGAGCTGAGCTGAGGAGGG 2594
Db 1627 ACTCGAGCTACGAGC-----AGTACGCGCTCATCTGAGGAGATCTGAGCTG 1633
Qy 2595 GCTGCGGGCATAGGAGGAGGAGGAGCTGAGCTTGGAGAGATGGAGAAGACACTC 2654
Db 1684 GCTGGCGCAGGAGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1743
Qy 2655 GCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2714
Db 1744 GCTGAGGAGGAGGAGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1803
Qy 2715 GCTGGAGGAGCTACAGGAGGCCATGGAGCTGAGCTACACTGGTCAATTGAG 2768

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 328:

SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 328:

US-10-084-843-328

Query Match 2.0%; Score 63.8; DB 15; Length 1166;
Best Local Similarity 26.7%; Pred. No. 2.2e-06;
Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;

Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;

Qy 2 TCTATATTCGACCTCTCTCTCATCTCTGCATCCAAAGAACACAGGCCCATCG 61
Db 373 KSAANTSMKGGTSTYCTWYTCNGGASTAMTYNMCCCCGWAAYCKSCWAWYCCCTCGTCA 432

Qy 62 CTTTCCTCCTCACACTCTCATCGACACGCCGCTCTCATCTACGGCTCATCG 121
Db 433 TYCCMCMCGSGSYCTTCAMNCACCCYTGNGAATGAGCTGGCTCGTCA 492

Qy 122 TCTCATGCCATCTCACACTCTCACACTCTGACCTGGGATACGGAGCTGGCTCGTCA 181
Db 493 TNTNMNCCSCNCNRYCTTCMNCNCKSGKACCNATMYCSACKHHTCTMCYMSACKMT 552

Qy 182 ACGCCTCTCATCTCACACTCTCACACTCTGACCTGGGATACGGAGCTGGCTCGTCA 181
Db 553 TCCCTCCTNCTYTNCCAMCMCSCTCTWCMAACTCKCCGGICKNCNCWCTCTKCCAY 612

Qy 242 TTTCATCCTACTCTGACTCTTACCCACACGGGCTTACCACTCTAGCTTAACTCTC 301
Db 613 NMACCKKKKHYCYNCWYCYMKCKCAGSYKNCMCCWACTCTMNTTCTCNKCCM 672

Qy 302 GACCAACCTCACCATCACCATCACATGTTCTCCATTAAGCTGAGCTCTCCA 241
Db 673 KACCKNNTCTCWSSCCCCACAKAYMCTAWCMNTTCCMCTKASSCCYYCNYCMM 732

Qy 362 GACCGCTGAACACTTATCACCTCAAGCTCTCTCATCGTTCAACACCGCTG 421
Db 733 CWCWTCTWNAKCANCNCTCTCTCTCMMYTMACKCWNNTCCKSGACCYCTCTCAC 792

Qy 422 CTCATATCCCTACGAAAGCTTGTATCACCTCTACTCATCACAGCTCACTGATCA 481
Db 793 TTKKCKKNTCTCTCTMCKCYYCNYCMM 852

Qy 482 GCAACCAAACCTCGACTCTCTCTGACTCTAGCTGACTGATCTCTCCACCA- 540
Db 853 YYAKKAENMCTCCANNCNCKTCKTCCCACMKSAACNCKCNCWCCCTCCATCG 912

Qy 541 TCTTCATCATCTCCCTACTCGACCAACGGTGCCTCTCGCTCCACCATTAAG 600
Db 913 TCTCWTCTATCTCKCTCWNCTYCNMCKACNCKYAYTCNACTMNWNCCANCNCTCT 972

Qy 601 CTCATCTGATGTCAGAAGAGAGAGAGTCAGCTCAACGCCGCACTCGACGCCGTT 660
Db 973 NYCTCWTCKAGCTYCKCKCTMCKCNMCHRNWTCTYRCTCKCNCNCRNCKMCKTCT 1032

Qy 661 CCCCTCTTACATCACCTGACCTGGCTTACCATCCACACCCGCT 711
Db 1033 CTCCWMKWTCCWCCATCTNMKSTCTCWNCNCMTCCTENKCCYNTKY 1083

US-11-028-898-328

Query Match 2.0%; Score 63.8; DB 24; Length 1166;
Best Local Similarity 26.7%; Pred. No. 2.2e-06;
Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;

Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;

Qy 2 TCTATATTCGACCTCTCTCATCTCTGCATCCAAAGAACACAGGCCCATCG 61
Db 373 KSAANTSMKGGTSTYCTWYTCNGGASTAMTYNMCCCCGWAAYCKSCWAWYCCCTCGTCA 432

Qy 62 CTTTCCTCCTCACACTCTCATCGACCCGGTCTCTCACTACTCGGCTCATCG 121
Db 433 TYCCMCMCGSGSYCTTCAMNCACCCYTGNGAATGAGCTGGCTCGTCA 492

Qy 122 TCTCATGCTCATCTCACACTCTGACCTGGGATACGGAGCTGGCTCGTCA 181
Db 493 TNTNMNCCSCNCNRYCTTCMNCNCKSGKACCNATMYCSACKHHTCTMCYMSACKMT 552

Qy 182 ACGCCTCTCATCTCACACTCTGACCTGGGATACGGAGCTGGCTCGTCA 241
Db 553 TCCCTCCTNCTYTNCCAMCMCSCTCTWCMAACTCKCCGGICKNCNCWCTCTKCCAY 612

Qy 242 TTTCATCCTACTCTGACTCTTACCCACACGGGCTTACCACTCTAGCTTAACTCTC 301

Publication No. US20050136069A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
Skiky, Yasir A.W.
Dillon, Davin C.
Campos Neto, Antonio
Houghton, Raymond
Vedwick, Thomas S.
Twardzik, Daniel R.
Loes, Michael J.
Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/1/028,898

FILING DATE: 03-Jan-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/084,843

FILING DATE: 03-Jan-2005

APPLICATION NUMBER: US/09/072,967

FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 328:

SEQUENCE CHARACTERISTICS:
LENGTH: 116 base Pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 328:

US-11-028-898-328

Query Match 2.0%; Score 63.8; DB 24; Length 1166;
Best Local Similarity 26.7%; Pred. No. 2.2e-06;
Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;

Matches 190; Conservative 136; Mismatches 384; Indels 1; Gaps 1;

Qy 2 TCTATATTCGACCTCTCTCATCTCTGCATCCAAAGAACACAGGCCCATCG 61
Db 373 KSAANTSMKGGTSTYCTWYTCNGGASTAMTYNMCCCCGWAAYCKSCWAWYCCCTCGTCA 432

Qy 62 CTTTCCTCCTCACACTCTCATCGACCCGGTCTCTCACTACTCGGCTCATCG 121
Db 433 TYCCMCMCGSGSYCTTCAMNCACCCYTGNGAATGAGCTGGCTCGTCA 492

Qy 122 TCTCATGCTCATCTCACACTCTGACCTGGGATACGGAGCTGGCTCGTCA 181
Db 493 TNTNMNCCSCNCNRYCTTCMNCNCKSGKACCNATMYCSACKHHTCTMCYMSACKMT 552

Qy 182 ACGCCTCTCATCTCACACTCTGACCTGGGATACGGAGCTGGCTCGTCA 241
Db 553 TCCCTCCTNCTYTNCCAMCMCSCTCTWCMAACTCKCCGGICKNCNCWCTCTKCCAY 612

Qy 242 TTTCATCCTACTCTGACTCTTACCCACACGGGCTTACCACTCTAGCTTAACTCTC 301

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